

SEQUENCE LISTING

<110> Alitalo, Kari
Joukov, Vladimir

<120> VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN
AND GENE, MUTANTS THEREOF, AND USES THEREOF

<130> 28967/34140A

<140>

<141>

<150> 09/355,700

<151> 1999-11-05

<150> PCT/US98/01973

<151> 1998-02-02

<150> 08/795,430

<151> 1997-02-05

<150> PCT/FI96/00427

<151> 1996-08-01

<150> 08/671,573

<151> 1996-06-28

<150> 08/601,132

<151> 1996-02-14

<150> 08/585,895

<151> 1996-01-12

<150> 08/510,133

<151> 1995-08-01

<150> 08/340,011

<151> 1994-11-14

<160> 59

<170> PatentIn Ver. 2.0

<210> 1

<211> 4416

<212> DNA

<213> Homo sapiens

<220>

<223> Human Flt4 cDNA (short form)

<400> 1

ccacgcgcag cggccggaga tgcagcgggg cgccgcgctg tgcctgcgac tgtggctctg 60

cctgggactc ctggacggcc tggtagtggt ctactccatg acccccccca ccttgaacat 120
cacggaggag tcacacgtca tcgacaccgg tgacagcctg tccatctcct gcaggggaca 180
gcacccccctc gagtgggctt ggccaggagc tcaggaggcg ccagccaccg gagacaagga 240
cagcgaggac acggggggtg tgcgagactg cgaggggcaca gacgccaggc cctactgcaa 300
ggtgttgctg ctgcacgagg tacatgccaa cgacacaggc agctacgtct gctactacaa 360
gtacatcaag gcacgcacg agggcaccac ggccgccagc tctacgtgt tcgtgagaga 420
ctttgagcag ccattcatca acaagcctga cacgctcttg gtcaacagga aggacgccat 480
gtgggtgccc tgtctggtgt ccatccccgg cctcaatgtc acgctgcgt cgcaaagctc 540
ggtgctgtgg ccagacgggc aggaggtggt gtgggatgac cggcggggca tgctcgtgtc 600
cacgccactg ctgcacgatg ccctgtacct gcagtgcgag accacctggg gagaccagga 660
cttcctttcc aaccttcc tgggtgcacat cacaggcaac gagctctatg acatccagct 720
gttgcccagg aagtcgtgg agctgctggt aggggagaag ctggctctga actgcaccgt 780
gtgggctgag ttttaactcag gtgtcacctt tgactgggac taccagggga agcaggcaga 840
gcggggtaag tgggtgccc agcgacgtc ccagcagacc cacacagaac tctccagcat 900
cctgaccatc cacaacgtca gccagcacga cctgggctcg tatgtgtgca aggccaacaa 960
cggcatccag cgatttcggg agagcaccga ggtcatttg catgaaaatc ccttcatcag 1020
cgctcagtggt ctcaaaggac ccatactgga ggccacggca ggagacgagc tgggtgaagct 1080
gcccgtaag ctggcagcgt accccccgcc cgagttccag tggtaaaagg atggaaaggc 1140
actgtccggg cgccacagtc cacatgccct ggtgctcaag gaggtgacag aggccagcac 1200
aggcacctac accctcgccc tgtggaactc cgctgctggc ctgaggcgca acatcagcct 1260
ggagctggtg gtgaatgtgc cccccagat acatgagaag gaggcctcct ccccagcat 1320
ctactcgtc cacagccgcc aggcctcac ctgcacggcc tacgggggtgc cctgcctct 1380
cagcatccag tggcactggc ggccctggac accctgcaag atgtttgccc agcgtagtct 1440
ccggcggcgg cagcagcaag acctcatgcc acagtgccgt gactggaggg cggtgaccac 1500
gcaggatgcc gtgaacccca tcgagagcct ggacacctgg accgagtttg tggagggaaa 1560
gaataagact gtgagcaagc tgggtgatcca gaatgccaac gtgtctgcca tgtacaagt 1620
tgtggctctc aacaagggtg gccaggatga gcggctcatc tacttctatg tgaccacat 1680
ccccgacggc ttcaccatcg aatccaagcc atccgaggag ctactagagg gccagccggt 1740

gctcctgagc tgccaagccg acagctacaa gtacgagcat ctgcgctggt accgcctcaa 1800
cctgtccacg ctgcacgatg cgcacgggaa cccgcttctg ctcgactgca agaactgtgca 1860
tctgttcgcc acccctctgg ccgccagcct ggaggaggtg gcacctgggg cgcgccacgc 1920
cacgctcagc ctgagtatcc cccgcgtcgc gcccgagcac gagggccact atgtgtgcga 1980
agtgcgaagac cggcgcagcc atgacaagca ctgccacaag aagtacctgt cgggtgcaggc 2040
cctggaagcc cctcggctca cgcagaactt gaccgacctc ctggtgaacg tgagcgactc 2100
gctggagatg cagtgccttg tggccggagc gcacgcgccc agcatcgtgt ggtacaaaga 2160
cgagaggctg ctggaggaaa agtctggagt cgacttggcg gactccaacc agaagctgag 2220
catccagcgc gtgcgcgagg aggatgcggg acgctatctg tgcagcgtgt gcaacgcca 2280
gggctgcgtc aactcctccg ccagcgtggc cgtggaaggc tccgaggata agggcagcat 2340
ggagatcgtg atccttgtcg gtaccggcgt catcgtgtc ttcttctggg tctcctcct 2400
cctcatcttc tgtaacatga ggaggccggc ccacgcagac atcaagacgg gctacctgtc 2460
catcatcatg gaccccgggg aggtgcctct ggaggagcaa tgcaataacc tgtctacga 2520
tgccagccag tgggaattcc cccgagagcg gctgcacctg gggagagtgc tcggctacgg 2580
cgccttcggg aaggtggtgg aagcctccgc ttccggcatc cacaaggga gcagctgtga 2640
cacctggcc gtgaaaatgc tgaaagagg cgccacggcc agcgagcacc gcgcgctgat 2700
gtcggagctc aagatcctca ttcacatcgg caaccacctc aacgtggtca acctcctcgg 2760
ggcgtgcacc aagccgcagg gcccctcat ggtgatcgtg gatttctgca agtacggcaa 2820
cctctccaac ttctgcgcg ccaagcggga cgccttcagc ccctgcgcgg agaagtctcc 2880
cgagcagcgc ggacgcttcc gcgccatggt ggagctcgcc aggctggatc ggaggcggcc 2940
ggggagcagc gacagggctc tcttcgcgcg gttctcgaag accgagggcg gagcgaggcg 3000
ggcttctcca gaccaagaag ctgaggacct gtggctgagc ccgctgacca tggaagatct 3060
tgtctgctac agcttccagg tggccagagg gatggagttc ctggcttccc gaaagtgcac 3120
ccacagagac ctggctgctc ggaacattct gctgtcggaa agcgacgtgg tgaagatctg 3180
tgactttggc cttgcccggg acatctacaa agacctgac tacgtccgca agggcagtgc 3240
ccggtgccc ctgaagtga tggccctga aagcatcttc gacaaggtgt acaccacgca 3300
gagtgcgtg tggctcttg ggggtgcttct ctgggagatc ttctctctgg gggcctcccc 3360
gtacctggg gtgcagatca atgaggagtt ctgccagcg ctgagagacg gcacaaggat 3420

gagggccccc gagctggcca ctcccgccat acgcgcgcatc atgctgaact gctgggtccgg 3480
 agaccccaag gcgagacctg cattctcgga gctgggtggag atcctggggg acctgctcca 3540
 gggcagggggc ctgcaagagg aagaggaggt ctgcatggcc ccgcgcagct ctcaagagctc 3600
 agaagagggc agcttctcgc aggtgtccac catggcccta cacatcgccc aggctgacgc 3660
 tgaggacagc ccgccaagcc tgcagcgcca cagcctggcc gccaggtatt acaactgggt 3720
 gtcccttccc ggggtgcctgg ccagaggggc tgagaccctg ggttccctca ggatgaagac 3780
 atttgaggaa ttcccatga cccaacgac ctacaaaggc tctgtggaca accagacaga 3840
 cagtgggatg gtgctggcct cggaggaggt tgagcagata gagagcaggc atagacaaga 3900
 aagcggcttc aggtagctga agcagagaga gagaaggcag catacgtcag cattttcttc 3960
 tctgcactta taagaaagat caaagacttt aagactttcg ctatttcttc tactgctatc 4020
 tactacaaac ttcaaagagg aaccaggagg acaagaggag catgaaagtg gacaaggagt 4080
 gtgaccactg aagcaccaca gggaaggggt taggcctccg gatgactgcg ggcaggcctg 4140
 gataatatcc agcctccac aagaagctgg tggagcagag tgttccctga ctccctcaag 4200
 gaaagggaga cgccctttca tgggtctgctg agtaacaggt gcnttcccag aactggcgt 4260
 tactgcttga ccaaagagcc ctcaagcggc ccttatgcc a gctgacaga gggctcacct 4320
 cttgccttct aggtcacttc tcacacaatg tcccttcagc acctgaccct gtgcccgcga 4380
 gttattcctt ggtaatatga gtaatacatc aaagag 4416

<210> 2

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<223> Human Flt4 cDNA (3' end-long form)

<400> 2

caagaaagcg gcttcagctg taaaggacct ggccagaatg tggctgtgac cagggcacac 60
 cctgactccc aaggaggcg gcggcgccct gagcggggggg cccgaggagg ccaggtgttt 120
 tacaacagcg agtatgggga gctgtcggag ccaagcgagg aggaccactg ctccccgtct 180
 gcccgcgtga ctttcttcac agacaacagc tactaa 216

<210> 3

<211> 4273

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pLTRpoly
vector

<400> 3

aagcttatcg atttcgaacc cggggtacc gaattcctcg agtctagagg agcatgcctg 60
caggctcgacc gggctcgatc ccctcgcgag ttggttcagc tgctgcctga ggctggacga 120
cctcgcgag ttctaccggc agtgcaaacc cgctcgcatc caggaaacca gcagcggcta 180
tccgcgcatc catgcccccg aactgcagga gtggggaggc acgatggccg ctttgggtccc 240
ggatctttgt gaaggaacct tacttctgtg gtgtgacata attggacaaa ctacctacag 300
agatttaaag ctctaaggta aatataaaat ttttaagtgt ataattgtgt aaactactga 360
ttctaattgt ttgtgtatct tagattccaa cctatggaac tgatgaatgg gagcagtggg 420
ggaatgcctt taatgaggaa aacctgtttt gctcagaaga aatgccatct agtgatgatg 480
aggctactgc tgactctcaa cattctactc ctccaaaaaa gaagagaaaag gtagaagacc 540
ccaaggactt tccttcagaa ttgctaagtt ttttgagtca tgctgtgttt agtaatagaa 600
ctcttgcttg ctttgctatt tacaccacaa aggaaaaagc tgcactgcta tacaagaaaa 660
ttatggaaaa atattctgta acctttataa gtaggcataa cagttataat cataacatac 720
tggtttttct tactccacac aggcatagag tgtctgctat taataactat gctcaaaaat 780
tgtgtacctt tagcttttta atttgtaaag gggttaataa ggaatatttg atgtatagtg 840
ccttgactag agatcataat cagccatacc acattttag aggttttact tgctttaaaa 900
aacctcccac acctccccct gaacctgaaa cataaaatga atgcaattgt tgttgttaac 960
ttgtttattg cagcttataa tggttacaaa taaagcaata gcatcacaaa tttcacaaat 1020
aaagcatttt tttcactgca ttctagttgt ggtttgtcca aactcatcaa tgtatcttat 1080
catgtctgga tctgcccgtc tccctatagt gagtcgtatt aatttcgata agccagggtta 1140
acctgcatta atgaatcggc caacgcgcgg ggagaggcgg tttgcgtatt gggcgctctt 1200
ccgcttcctc gctcactgac tcgctgcgct cggctcggtc gctgcggcga gcggtatcag 1260
ctcactcaaa ggcggttaata cggttatcca cagaatcagg ggataacgca ggaaagaaca 1320
tgtgagcaaa aggccagcaa aaggccagga accgtaaaaa ggacgcgttg ctggcgtttt 1380
tccataggct ccgccccctt gacgagcatc acaaaaaatcg acgctcaagt cagaggtggc 1440

gaaacccgac aggactataa agataccagg cgtttccccc tggaagctcc ctctgtcgct 1500
ctctgtttcc gaccctgccg cttaccggat acctgtccgc ctttctccct tcgggaagcg 1560
tggcgctttc tcaatgctca cgctgtaggt atctcagttc ggtgtaggtc gttcgctcca 1620
agctgggctg tgtgcacgaa cccccgttc agcccgaccg ctgcgcctta tccggtaact 1680
atcgtcttga gtccaacccg gtaagacacg acttatcgcc actggcagca gccactggta 1740
acaggattag cagagcgagg tatgtaggcg gtgctacaga gttcttgaag tgggtggccta 1800
actacggcta cactagaagg acagtatttg gtatctgcgc tctgctgaag ccagttacct 1860
tcggaaaaag agttggtagc tcttgatccg gcaaacaaac caccgctggg agcggtggtt 1920
tttttgtttg caagcagcag attacgcgca gaaaaaaagg atctcaagaa gatcctttga 1980
tcttttctac ggggtctgac gctcagtggg acgaaaactc acgttaaggg attttggtca 2040
tgagattatc aaaaaggatc ttcacctaga tccttttaaa ttaaaaatga agttttaaat 2100
caatctaaag tatatatgag taaacttggg ctgacagtta ccaatgctta atcagtgagg 2160
cacctatctc agcgatctgt ctatttcgtt catccatagt tgctgactc cccgtcgtgt 2220
agataactac gatacgggag ggcttaccat ctggccccag tgctgcaatg ataccgcgag 2280
accacgctc accggtcca gatttatcag caataaacca gccagccgga agggccgagc 2340
gcagaagtgg tcctgcaact ttatccgcct ccattccagtc tattaattgt tgccgggaag 2400
ctagagtaag tagttcgcca gttaatagtt tgcgcaacgt tgttgccatt gctacaggca 2460
tcgtggtgtc acgctcgtcg tttgggatgg cttcattcag ctccggttcc caacgatcaa 2520
ggcgagttac atgatcccc atgttggtgca aaaaagcggg tagctccttc ggtcctccga 2580
tcgttgctcag aagtaagttg gccgcagtgt tatcactcat ggttatggca gcactgcata 2640
attctcttac tgtcatgcca tccgtaagat gcttttctgt gactgggtgag tactcaacca 2700
agtcattctg agaatagtgt atgcggcgac cgagttgctc ttgcccggcg tcaatacggg 2760
ataataccgc gccacatagc agaactttaa aagtgtcat cattggaaaa cgttcttcgg 2820
ggcgaaaact ctcaaggatc ttaccgctgt tgagatccag ttcgatgtaa cccactcgtg 2880
caccacaactg atcttcagca tcttttactt tcaccagcgt ttctgggtga gcaaaaacag 2940
gaaggcaaaa tgccgcaaaa aagggaataa gggcgacacg gaaatgttga atactcatac 3000
tcttcctttt tcaatattat tgaagcattt atcagggtta ttgtctcatg agcggataca 3060
tatttgaatg tatttagaaa aataaacaaa taggggttcc gcgcacattt ccccgaagg 3120

tgccacctga cgtctaagaa accattatta tcatgacatt aacctataaa aataggcgta 3180
 tcacgaggcc ctttcgtctc gcgcgtttcg gtgatgacgg tgaaaacctc tgacacatgc 3240
 agtccccgga gacggtcaca gcttgtctgt aagcggatgc cgggagcaga caagcccgtc 3300
 agggcgcgtc agcgggtggt ggcgggtgtc ggggctggct taactatgcg gcatcagagc 3360
 agattgtact gagagtgcac catatggaca tattgtcggt agaacgcggc tacaattaat 3420
 acataacctt atgtatcata cacatacgat ttaggtgaca ctatagaact cgagcagagc 3480
 ttccaaattg agagagaggc ttaatcagag acagaaaactg tttgagtcaa ctcaaggatg 3540
 gtttgaggga ctgtttaaca gatccccttg gtttaccacc ttgatatcta ccattatggg 3600
 acccctcatt gtactcctaa tgattttgct cttcggacct tgcattctta atcgattagt 3660
 ccaatttggt aaagacagga tatcagtggc ccaggctcta gttttgactc aacaatatca 3720
 ccagctgaag cctatagagt acgagccata gataaaataa aagattttat ttagtctcca 3780
 gaaaaagggg ggaatgaaag accccacctg taggtttggc agctagctt aagtaacgcc 3840
 attttgcaag gcatggaaaa atacataact gagaatagag aagttcagat caaggtcagg 3900
 aacagatgga acagctgaat atgggccaaa caggatatct gtggttagca gttcctgccc 3960
 cggtcagggg ccaagaacag atggaacagc tgaatatggg ccaaacagga tatctgtggc 4020
 aagcagttcc tgccccggct cagggccacg aacagatggt cccagatgc ggtccagccc 4080
 tcagcagttt ctagagaacc atcagatggt tccagggtgc cccaaggacc tgaaatgacc 4140
 ctgtgcctta tttgaactaa ccaatcagtt cgcttctcgc ttctgttcgc gcgcttctgc 4200
 tccccgagct caataaaaga gccacaacc cctcactcgg ggcgccagtc ctccgattga 4260
 ctgagtcgcc cgg

4273

<210> 4
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Flt4 c-terminal peptide

<400> 4
 Pro Met Thr Pro Thr Thr Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp
 1 5 10 15
 Ser Gly Met Val Leu Ala Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg
 20 25 30

His Arg Gln Glu Ser Gly Phe Arg
35 40

<210> 5
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<223> At position 1, Xaa = Unknown

<220>
<223> N-terminal sequence from VEGF-C purified from PC-3
conditioned medium

<400> 5
Xaa Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile
1 5 10 15

Leu Lys

<210> 6
<211> 219
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: vector and
human VEGF-C cDNA

<400> 6
tcactatagg gagaccaag cttggtaccg agctcggatc cactagtaac ggccgccagt 60
gtggtggaat tcgacgaact catgactgta ctctaccag aatattggaa aatgtacaag 120
tgtcagctaa ggcaaggagg ctggcaacat aacagagaac aggccaacct caactcaagg 180
acagaagaga ctataaaatt cgctgcagca cactacaac 219

<210> 7
<211> 1997
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (352)..(1608)

<220>
<223> prepro VEGF-C cDNA


```

<400> 7
cccccccgcc ctctccaaaa agctacaccg acgcggaccg cggcggcgctc ctccctcgcc 60
ctcgcttcac ctgcggggct ccgaatgcgg ggagctcgga tgtccggttt cctgtgagggc 120
ttttacctga caccgcgcgc ctttccccgg cactggctgg gaggggcgccc tgcaaagttg 180
ggaacgcgga gccccggacc cgctcccgcc gctccgggt cgcccagggg gggctgcgcgg 240
gaggagcccc ggggagaggg accaggaggg gcccgcggcc tcgcaggggc gcccgcgccc 300
ccaccctgc ccccgccagc ggaccgggtcc cccacccccg gtccttcac c atg cac 357
                                     Met His
                                     1
ttg ctg ggc ttc ttc tct gtg gcg tgt tct ctg ctc gcc gct gcg ctg 405
Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala Ala Leu
      5                      10                      15
ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc gcc gcc ttc gag tcc 453
Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe Glu Ser
      20                      25                      30
gga ctc gac ctc tcg gac gcg gag ccc gac gcg ggc gag gcc acg gct 501
Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
      35                      40                      45                      50
tat gca agc aaa gat ctg gag gag cag tta cgg tct gtg tcc agt gta 549
Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
      55                      60                      65
gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 597
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
      70                      75                      80
tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac 645
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
      85                      90                      95
ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat 693
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr
      100                      105                      110
aat aca gag atc ttg aaa agt att gat aat gag tgg aga aag act caa 741
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln
      115                      120                      125                      130
tgc atg cca cgg gag gtg tgt ata gat gtg ggg aag gag ttt gga gtc 789
Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val
      135                      140                      145
gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt 837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys
      150                      155                      160

```

ggg ggt tgc tgc aat agt gag ggg ctg cag tgc atg aac acc agc acg	885
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr	
165 170 175	
agc tac ctc agc aag acg tta ttt gaa att aca gtg cct ctc tct caa	933
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln	
180 185 190	
ggc ccc aaa cca gta aca atc agt ttt gcc aat cac act tcc tgc cga	981
Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg	
195 200 205 210	
tgc atg tct aaa ctg gat gtt tac aga caa gtt cat tcc att att aga	1029
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg	
215 220 225	
cgt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc	1077
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr	
230 235 240	
tgc ccc acc aat tac atg tgg aat aat cac atc tgc aga tgc ctg gct	1125
Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala	
245 250 255	
cag gaa gat ttt atg ttt tcc tcg gat gct gga gat gac tca aca gat	1173
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp	
260 265 270	
gga ttc cat gac atc tgt gga cca aac aag gag ctg gat gaa gag acc	1221
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr	
275 280 285 290	
tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct gcc agc tgt gga ccc	1269
Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro	
295 300 305	
cac aaa gaa cta gac aga aac tca tgc cag tgt gtc tgt aaa aac aaa	1317
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys	
310 315 320	
ctc ttc ccc agc caa tgt ggg gcc aac cga gaa ttt gat gaa aac aca	1365
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr	
325 330 335	
tgc cag tgt gta tgt aaa aga acc tgc ccc aga aat caa ccc cta aat	1413
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn	
340 345 350	
cct gga aaa tgt gcc tgt gaa tgt aca gaa agt cca cag aaa tgc ttg	1461
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu	
355 360 365 370	
tta aaa gga aag aag ttc cac cac caa aca tgc agc tgt tac aga cgg	1509
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg	
375 380 385	

cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt 1557
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser
390 395 400

gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg aaa aga cca caa atg 1605
Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met
405 410 415

agc taagattgta ctgttttcca gttcatcgat tttctattat ggaaaactgt 1658
Ser

gttgccacag tagaactgtc tgtgaacaga gagacccttg tgggtccatg ctaacaaaga 1718
caaaagtctg tctttcctga accatgtgga taactttaca gaaatggact ggagctcatc 1778
tgcaaaaggc ctcttgtaaa gactgggttt ctgccaatga ccaaacagcc aagattttcc 1838
tcttgatgatt tctttaaaag aatgactata taatttattt ccactaaaaa tattgtttct 1898
gcattcattt ttatagcaac aacaattggt aaaactcact gtgatcaata tttttatatt 1958
atgcaaaaata tgttttaaata aaaatgaaaa ttgtattat 1997

<210> 8
<211> 419
<212> PRT
<213> Homo sapiens

<400> 8
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe
20 25 30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
405 410 415

Gln Met Ser

<210> 9
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<223> VEGF-C peptide "PAM126"

<400> 9
Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu
1 5 10 15

Lys

<210> 10
<211> 1836
<212> DNA
<213> Murine

<220>
<221> CDS
<222> (168) .. (1412)

<220>
<223> cDNA encoding murine VEGF-C precursor

<400> 10
gcggccgcgt cgacgcaaaa gttgctgagcc gccgagtcctc gggagacgct cgcccagggg 60
ggccccggg aggaaccac gggacagga ccaggagagg acctcagcct cagccccag 120
cctgcgccag ccaacggacc ggctccctg ctcccggtcc atccacc atg cac ttg 176
Met His Leu
1
ctg tgc ttc ttg tct ctg gcg tgt tcc ctg ctc gcc gct gcg ctg atc 224
Leu Cys Phe Leu Ser Leu Ala Cys Ser Leu Leu Ala Ala Ala Leu Ile
5 10 15
ccc agt ccg cgc gag gcg ccc gcc acc gtc gcc gcc ttc gag tcg gga 272
Pro Ser Pro Arg Glu Ala Pro Ala Thr Val Ala Ala Phe Glu Ser Gly
20 25 30 35
ctg ggc ttc tcg gaa gcg gag ccc gac ggg ggc gag gtc aag gct ttt 320
Leu Gly Phe Ser Glu Ala Glu Pro Asp Gly Gly Glu Val Lys Ala Phe
40 45 50

gaa ggc aaa gac ctg gag gag cag ttg cgg tct gtg tcc agc gta gat	368
Glu Gly Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val Asp	
55 60 65	
gag ctg atg tct gtc ctg tac cca gac tac tgg aaa atg tac aag tgc	416
Glu Leu Met Ser Val Leu Tyr Pro Asp Tyr Trp Lys Met Tyr Lys Cys	
70 75 80	
cag ctg cgg aaa ggc ggc tgg cag cag ccc acc ctc aat acc agg aca	464
Gln Leu Arg Lys Gly Gly Trp Gln Gln Pro Thr Leu Asn Thr Arg Thr	
85 90 95	
ggg gac agt gta aaa ttt gct gct gca cat tat aac aca gag atc ctg	512
Gly Asp Ser Val Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu	
100 105 110 115	
aaa agt att gat aat gag tgg aga aag act caa tgc atg cca cgt gag	560
Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu	
120 125 130	
gtg tgt ata gat gtg ggg aag gag ttt gga gca gcc aca aac acc ttc	608
Val Cys Ile Asp Val Gly Lys Glu Phe Gly Ala Ala Thr Asn Thr Phe	
135 140 145	
ttt aaa cct cca tgt gtg tcc gtc tac aga tgt ggg ggt tgc tgc aac	656
Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn	
150 155 160	
agc gag ggg ctg cag tgc atg aac acc agc aca ggt tac ctc agc aag	704
Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Gly Tyr Leu Ser Lys	
165 170 175	
acg ttg ttt gaa att aca gtg cct ctc tca caa ggc ccc aaa cca gtc	752
Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys Pro Val	
180 185 190 195	
aca atc agt ttt gcc aat cac act tcc tgc cgg tgc atg tct aaa ctg	800
Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu	
200 205 210	
gat gtt tac aga caa gtt cat tca att att aga cgt tct ctg cca gca	848
Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu Pro Ala	
215 220 225	
aca tta cca cag tgt cag gca gct aac aag aca tgt cca aca aac tat	896
Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr	
230 235 240	
gtg tgg aat aac tac atg tgc cga tgc ctg gct cag cag gat ttt atc	944
Val Trp Asn Asn Tyr Met Cys Arg Cys Leu Ala Gln Gln Asp Phe Ile	
245 250 255	
ttt tat tca aat gtt gaa gat gac tca acc aat gga ttc cat gat gtc	992
Phe Tyr Ser Asn Val Glu Asp Asp Ser Thr Asn Gly Phe His Asp Val	
260 265 270 275	

tgt gga ccc aac aag gag ctg gat gaa gac acc tgt cag tgt gtc tgc 1040
 Cys Gly Pro Asn Lys Glu Leu Asp Glu Asp Thr Cys Gln Cys Val Cys
 280 285 290

aag ggg ggg ctt cgg cca tct agt tgt gga ccc cac aaa gaa cta gat 1088
 Lys Gly Gly Leu Arg Pro Ser Ser Cys Gly Pro His Lys Glu Leu Asp
 295 300 305

aga gac tca tgt cag tgt gtc tgt aaa aac aaa ctt ttc cct aat tca 1136
 Arg Asp Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Asn Ser
 310 315 320

tgt gga gcc aac agg gaa ttt gat gag aat aca tgt cag tgt gta tgt 1184
 Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys
 325 330 335

aaa aga acg tgt cca aga aat cag ccc ctg aat cct ggg aaa tgt gcc 1232
 Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala
 340 345 350 355

tgt gaa tgt aca gaa aac aca cag aag tgc ttc ctt aaa ggg aag aag 1280
 Cys Glu Cys Thr Glu Asn Thr Gln Lys Cys Phe Leu Lys Gly Lys Lys
 360 365 370

ttc cac cat caa aca tgc agt tgt tac aga aga ccg tgt gcg aat cga 1328
 Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Ala Asn Arg
 375 380 385

ctg aag cat tgt gat cca gga ctg tcc ttt agt gaa gaa gta tgc cgc 1376
 Leu Lys His Cys Asp Pro Gly Leu Ser Phe Ser Glu Glu Val Cys Arg
 390 395 400

tgt gtc cca tcg tat tgg aaa agg cca cat ctg aac taagatcata 1422
 Cys Val Pro Ser Tyr Trp Lys Arg Pro His Leu Asn
 405 410 415

ccagttttca gtcagtcaca gtcatttact ctcttgaaga ctgttggaac agcacttagc 1482

actgtctatg cacagaaaga ctctgtggga ccacatggta acagaggccc aagtctgtgt 1542

ttattgaacc atgtggatta ctgcgggaga ggactggcac tcatgtgcaa aaaaaacctc 1602

ttcaaagact ggttttctgc cagggaccag acagctgagg tttttctctt gtgatttata 1662

aaaagaatga ctatataatt tatttccact aaaaatattg ttctgtcatt catttttata 1722

gcaataacaa ttggtaaagc tcaactgtgat cagtattttt ataacatgca aaactatggt 1782

taaaataaaa tgaaaattgt attataaaaa aaaaaaaaaa aaaaaaaaaa gctt 1836

<210> 11
 <211> 415
 <212> PRT
 <213> Murine

<400> 11
Met His Leu Leu Cys Phe Leu Ser Leu Ala Cys Ser Leu Leu Ala Ala
1 5 10 15
Ala Leu Ile Pro Ser Pro Arg Glu Ala Pro Ala Thr Val Ala Ala Phe
20 25 30
Glu Ser Gly Leu Gly Phe Ser Glu Ala Glu Pro Asp Gly Gly Glu Val
35 40 45
Lys Ala Phe Glu Gly Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60
Ser Val Asp Glu Leu Met Ser Val Leu Tyr Pro Asp Tyr Trp Lys Met
65 70 75 80
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln Gln Pro Thr Leu Asn
85 90 95
Thr Arg Thr Gly Asp Ser Val Lys Phe Ala Ala Ala His Tyr Asn Thr
100 105 110
Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met
115 120 125
Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Ala Ala Thr
130 135 140
Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly
145 150 155 160
Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Gly Tyr
165 170 175
Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro
180 185 190
Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met
195 200 205
Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser
210 215 220
Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro
225 230 235 240
Thr Asn Tyr Val Trp Asn Asn Tyr Met Cys Arg Cys Leu Ala Gln Gln
245 250 255
Asp Phe Ile Phe Tyr Ser Asn Val Glu Asp Asp Ser Thr Asn Gly Phe
260 265 270
His Asp Val Cys Gly Pro Asn Lys Glu Leu Asp Glu Asp Thr Cys Gln
275 280 285

Cys Val Cys Lys Gly Gly Leu Arg Pro Ser Ser Cys Gly Pro His Lys
290 295 300

Glu Leu Asp Arg Asp Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe
305 310 315 320

Pro Asn Ser Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln
325 330 335

Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly
340 345 350

Lys Cys Ala Cys Glu Cys Thr Glu Asn Thr Gln Lys Cys Phe Leu Lys
355 360 365

Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys
370 375 380

Ala Asn Arg Leu Lys His Cys Asp Pro Gly Leu Ser Phe Ser Glu Glu
385 390 395 400

Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro His Leu Asn
405 410 415

<210> 12
<211> 1741
<212> DNA
<213> Quail

<220>
<221> CDS
<222> (453)..(1706)

<220>
<223> Quail VEGF-C cDNA

<400> 12
gccccgcgcg agcgctccgc gcgcagccgc cgggcccgggc cggcccgcgcg agggcgcgct 60
gcgagcggcc actgggtcct gcttccctcc ttcctctccc tctctctcct cctccttctc 120
tctgcgcttt ccaccgctcc cgagcgagcg cacgctcgga tgtccggttt cctgggtgggt 180
tttttacctg gcaaagtccg gataacttcg gtgagaattt gcaaagagggc tgggagctcc 240
cctgcaggcg tctgggagct gctgccgcgc tgcattcttc tccatcccgc ggattttact 300
gccttgata ttgcgagggg agggaggggg gtgaggacag caaaaagaaa ggggtggggg 360
gggggagaga aaaggaaaag aaggagcctc ggaattgtgc ccgcattcct gcgctgcccc 420
ggggccccc tccgctctgc catctccgca ca atg cac ttg ctg gag atg ctc 473
Met His Leu Leu Glu Met Leu

tcc ctg ggc tgc tgc ctc gct gct ggc gcc gtg ctc ctg gga ccc cgg	521
Ser Leu Gly Cys Cys Leu Ala Ala Gly Ala Val Leu Leu Gly Pro Arg	
10 15 20	
cag ccg ccc gtc gcc gcc gcc tac gag tcc ggg cac ggc tac tac gag	569
Gln Pro Pro Val Ala Ala Ala Tyr Glu Ser Gly His Gly Tyr Tyr Glu	
25 30 35	
gag gag ccc ggt gcc ggg gaa ccc aag gct cat gca agc aaa gac ctg	617
Glu Glu Pro Gly Ala Gly Glu Pro Lys Ala His Ala Ser Lys Asp Leu	
40 45 50 55	
gaa gag cag ttg cga tct gtg tcc agt gtg gat gaa ctc atg aca gta	665
Glu Glu Gln Leu Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val	
60 65 70	
ctt tac cca gaa tac tgg aaa atg ttc aaa tgt cag ttg agg aaa gga	713
Leu Tyr Pro Glu Tyr Trp Lys Met Phe Lys Cys Gln Leu Arg Lys Gly	
75 80 85	
ggg tgg caa cac aac agg gaa cac tcc agc tct gat aca aga tca gat	761
Gly Trp Gln His Asn Arg Glu His Ser Ser Ser Asp Thr Arg Ser Asp	
90 95 100	
gat tca ttg aaa ttt gcc gca gca cat tat aat gca gag atc ctg aaa	809
Asp Ser Leu Lys Phe Ala Ala Ala His Tyr Asn Ala Glu Ile Leu Lys	
105 110 115	
agt att gat act gaa tgg aga aaa acc cag ggc atg cca cgt gaa gtg	857
Ser Ile Asp Thr Glu Trp Arg Lys Thr Gln Gly Met Pro Arg Glu Val	
120 125 130 135	
tgt gtg gat ttg ggg aaa gag ttt gga gca act aca aac acc ttc ttt	905
Cys Val Asp Leu Gly Lys Glu Phe Gly Ala Thr Thr Asn Thr Phe Phe	
140 145 150	
aaa ccc ccg tgt gta tcc atc tac aga tgt gga ggt tgc tgc aat agt	953
Lys Pro Pro Cys Val Ser Ile Tyr Arg Cys Gly Gly Cys Cys Asn Ser	
155 160 165	
gaa gga ctc cag tgt atg aat atc agc aca aat tac atc agc aag aca	1001
Glu Gly Leu Gln Cys Met Asn Ile Ser Thr Asn Tyr Ile Ser Lys Thr	
170 175 180	
ttg ttt gag att aca gtg cct ctc tct cat ggc ccc aaa cct gta aca	1049
Leu Phe Glu Ile Thr Val Pro Leu Ser His Gly Pro Lys Pro Val Thr	
185 190 195	
gtc agt ttt gcc aat cac acg tcc tgc cga tgc atg tct aag ttg gat	1097
Val Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp	
200 205 210 215	
ggt tac aga caa gtt cat tct atc ata aga cgt tcc ttg cca gca aca	1145
Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr	
220 225 230	

caa act cag tgt cat gtg gca aac aag acc tgt cca aaa aat cat gtc 1193
 Gln Thr Gln Cys His Val Ala Asn Lys Thr Cys Pro Lys Asn His Val
 235 240 245

tgg aat aat cag att tgc aga tgc tta gca cag cac gat ttt ggt ttc 1241
 Trp Asn Asn Gln Ile Cys Arg Cys Leu Ala Gln His Asp Phe Gly Phe
 250 255 260

tct tct cac ctt gga gat tct gac aca tct gaa gga ttc cat att tgt 1289
 Ser Ser His Leu Gly Asp Ser Asp Thr Ser Glu Gly Phe His Ile Cys
 265 270 275

ggg ccc aac aaa gag ctg gat gaa gaa acc tgt caa tgc gtc tgc aaa 1337
 Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Lys
 280 285 290 295

gga ggt gtg cgg ccc ata agc tgt ggc cct cac aaa gaa cta gac agg 1385
 Gly Gly Val Arg Pro Ile Ser Cys Gly Pro His Lys Glu Leu Asp Arg
 300 305 310

gca tca tgt cag tgc atg tgc aaa aac aaa ctg ctc ccc agt tcc tgt 1433
 Ala Ser Cys Gln Cys Met Cys Lys Asn Lys Leu Leu Pro Ser Ser Cys
 315 320 325

ggg cct aac aaa gaa ttt gat gaa gaa aag tgc cag tgt gta tgt aaa 1481
 Gly Pro Asn Lys Glu Phe Asp Glu Glu Lys Cys Gln Cys Val Cys Lys
 330 335 340

aag acc tgt ccc aaa cat cat cca cta aat cct gca aaa tgc atc tgc 1529
 Lys Thr Cys Pro Lys His His Pro Leu Asn Pro Ala Lys Cys Ile Cys
 345 350 355

gaa tgt aca gaa tct ccc aat aaa tgt ttc tta aaa gga aaa aga ttt 1577
 Glu Cys Thr Glu Ser Pro Asn Lys Cys Phe Leu Lys Gly Lys Arg Phe
 360 365 370 375

cat cac cag aca tgc agt tgt tac aga cca cca tgt aca gtc cga acg 1625
 His His Gln Thr Cys Ser Cys Tyr Arg Pro Pro Cys Thr Val Arg Thr
 380 385 390

aaa cgc tgt gat gct gga ttt ctg tta gct gaa gaa gtg tgc cgc tgt 1673
 Lys Arg Cys Asp Ala Gly Phe Leu Leu Ala Glu Glu Val Cys Arg Cys
 395 400 405

gta cgc aca tct tgg aaa aga cca ctt atg aat taagcgaaga aagcactact 1726
 Val Arg Thr Ser Trp Lys Arg Pro Leu Met Asn
 410 415

cgctatatag tgtcg 1741

<210> 13
 <211> 418
 <212> PRT
 <213> Quail

<400> 13

Met His Leu Leu Glu Met Leu Ser Leu Gly Cys Cys Leu Ala Ala Gly
1 5 10 15

Ala Val Leu Leu Gly Pro Arg Gln Pro Pro Val Ala Ala Ala Tyr Glu
20 25 30

Ser Gly His Gly Tyr Tyr Glu Glu Glu Pro Gly Ala Gly Glu Pro Lys
35 40 45

Ala His Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser
50 55 60

Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Phe
65 70 75 80

Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu His Ser
85 90 95

Ser Ser Asp Thr Arg Ser Asp Asp Ser Leu Lys Phe Ala Ala Ala His
100 105 110

Tyr Asn Ala Glu Ile Leu Lys Ser Ile Asp Thr Glu Trp Arg Lys Thr
115 120 125

Gln Gly Met Pro Arg Glu Val Cys Val Asp Leu Gly Lys Glu Phe Gly
130 135 140

Ala Thr Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Ile Tyr Arg
145 150 155 160

Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Ile Ser
165 170 175

Thr Asn Tyr Ile Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser
180 185 190

His Gly Pro Lys Pro Val Thr Val Ser Phe Ala Asn His Thr Ser Cys
195 200 205

Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile
210 215 220

Arg Arg Ser Leu Pro Ala Thr Gln Thr Gln Cys His Val Ala Asn Lys
225 230 235 240

Thr Cys Pro Lys Asn His Val Trp Asn Asn Gln Ile Cys Arg Cys Leu
245 250 255

Ala Gln His Asp Phe Gly Phe Ser Ser His Leu Gly Asp Ser Asp Thr
260 265 270

Ser Glu Gly Phe His Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu
275 280 285

Thr Cys Gln Cys Val Cys Lys Gly Gly Val Arg Pro Ile Ser Cys Gly
 290 295 300

Pro His Lys Glu Leu Asp Arg Ala Ser Cys Gln Cys Met Cys Lys Asn
 305 310 315 320

Lys Leu Leu Pro Ser Ser Cys Gly Pro Asn Lys Glu Phe Asp Glu Glu
 325 330 335

Lys Cys Gln Cys Val Cys Lys Lys Thr Cys Pro Lys His His Pro Leu
 340 345 350

Asn Pro Ala Lys Cys Ile Cys Glu Cys Thr Glu Ser Pro Asn Lys Cys
 355 360 365

Phe Leu Lys Gly Lys Arg Phe His His Gln Thr Cys Ser Cys Tyr Arg
 370 375 380

Pro Pro Cys Thr Val Arg Thr Lys Arg Cys Asp Ala Gly Phe Leu Leu
 385 390 395 400

Ala Glu Glu Val Cys Arg Cys Val Arg Thr Ser Trp Lys Arg Pro Leu
 405 410 415

Met Asn

<210> 14
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<220>
 <223> IgG-Kappa sequence

<400> 14
 Ala Val Val Met Thr Gln Thr Pro Ala Ser
 1 5 10

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 15
 tctcttctgt gcttgagttg ag

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 16
tctcttctgt ccctgagttg ag

22

<210> 17
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 17
tgtgctgcag caaatTTTat agtctcttct gtggcggcgg cggcggcggg cgcctcgcga 60
ggacc 65

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 18
ctggcaggga actgctaata atggaatgaa

30

<210> 19
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 19
gggctccgcg tccgagaggt cgagtccgga ctcgtgatgg tgatgggtgat gggcggcggc 60
ggcggcgggc gcctcgcgag gacc 84

<210> 20
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 20
gtattataat gtcctccacc aaattttata g 31

<210> 21
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 21
gttcgctgcc tgacactgtg gtagtggtgc tggcggccgc tagtgatggt gatggtgatg 60
aataatggaa tgaacttgtc tgtaaacatc cag 93

<210> 22
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 22
catgtacgaa ccgccag 17

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 23
aatgaccaga gagaggcgag 20

<210> 24
<211> 24

<212> DNA
<213> Homo sapiens

<400> 24
ggcgaggcca cggtaggtct gcgt

24

<210> 25
<211> 24
<212> DNA
<213> Homo sapiens

<400> 25
tttctttgac aggcttatgc aagc

24

<210> 26
<211> 24
<212> DNA
<213> Homo sapiens

<400> 26
gagatcttga aaagtaagta tggg

24

<210> 27
<211> 23
<212> DNA
<213> Homo sapiens

<400> 27
atgacttgac aggtattgat aat

23

<210> 28
<211> 23
<212> DNA
<213> Homo sapiens

<400> 28
ctcagcaaga cggtgggtat tgt

23

<210> 29
<211> 25
<212> DNA
<213> Homo sapiens

<400> 29
cccttctttg tagttatttg aaatt

25

<210> 30
<211> 27
<212> DNA

<213> Homo sapiens

<400> 30
acactaccac agtgagtatg aattaaa

27

<210> 31
<211> 24
<212> DNA
<213> Homo sapiens

<400> 31
ttctttccaaa ggtgtcaggc agcg

24

<210> 32
<211> 21
<212> DNA
<213> Homo sapiens

<400> 32
gctggagatg gtagcagaat g

21

<210> 33
<211> 23
<212> DNA
<213> Homo sapiens

<400> 33
ctatttgtct agactcaaca gat

23

<210> 34
<211> 22
<212> DNA
<213> Homo sapiens

<400> 34
caaacatgca ggtaagagat cc

22

<210> 35
<211> 24
<212> DNA
<213> Homo sapiens

<400> 35
tgttctccta gctgttacag acgg

24

<210> 36
<211> 24
<212> DNA
<213> Murine

<400> 36 ggcgaggtca aggtaggtgc aagg	24
<210> 37 <211> 26 <212> DNA <213> Murine	
<400> 37 attgtctttg acaggctttt tgaagg	26
<210> 38 <211> 21 <212> DNA <213> Murine	
<400> 38 gagatcctga aaagtaagta g	21
<210> 39 <211> 24 <212> DNA <213> Murine	
<400> 39 tgtgactcga caggtattga taat	24
<210> 40 <211> 20 <212> DNA <213> Murine	
<400> 40 ctcagcaaga cggtaggtat	20
<210> 41 <211> 25 <212> DNA <213> Murine	
<400> 41 ttgtcccttg tagttgtttg aaatt	25
<210> 42 <211> 20 <212> DNA <213> Murine	
<400> 42	

acattaccac agtgagtatg

20

<210> 43
<211> 26
<212> DNA
<213> Murine

<400> 43
gtctcccca aaggtgtcag gcagct

26

<210> 44
<211> 23
<212> DNA
<213> Murine

<400> 44
aatgttgaag atggttaagta aaa

23

<210> 45
<211> 16
<212> DNA
<213> Murine

<400> 45
tctagactca accaat

16

<210> 46
<211> 22
<212> DNA
<213> Murine

<400> 46
caaacatgca ggtaaggagt gt

22

<210> 47
<211> 24
<212> DNA
<213> Murine

<400> 47
ttttccccta gttgttacag aaga

24

<210> 48
<211> 2991
<212> DNA
<213> Homo sapiens

<220>
<223> Genomic DNA - Sequence upstream of VEGF-C coding

sequence

<400> 48

gttttaagta gagacggggt ttcaccaacg gttgaaaata tttatcatgg tctccctaag 60
atggacggtg ttagctagga tgggtctcgat ctctgacct catgatccac cgcctcggc 120
ctcccaaagt gctgggatta caggcgtgag ccaccgtgc cgaccaacct taagacaaac 180
aactactgca tgattgtttt tggagacctt ttttttattc aaataaattt ttgccagcat 240
tttctgactc aaagtatagc agcaggaaga taacactttt gtgagaaaaa agtttgaata 300
cagcttactg ctgtatttaa atgaaacagt agttaatatg atattaatat attttgata 360
tattttgagt ttgttgattt tccagtcttc acccgctgct aggcctgtgg gtgttgaaa 420
tgctgtgtt tctcaatttt gtttgctat tagaatctg atgtccaagc cttactccag 480
ttagaccagt taagccagaa aggcagaagg tgtactcaag catctgtttt ttcaaaatct 540
ccttttgtga tgccaagtgc aatcaaagtt tagaatcatt gtaatagcaa atgggtgaat 600
ggaaactcca ccttctattc aaatcctacc ccagtctgcc cttagctgtt ctcttttcac 660
agatctatca atgtctgaag ataactatgg caggctgac aaatatgcat agagcaggaa 720
gacagcaaga gagtgatata ctgaccatgt tccaaatcac aaaacatctc aacaggctag 780
atcatggacc gagtctgatg ggatggaatt tcataaagat acataaaaaa gcatcttgga 840
tacagtaaac ttaactccac aaatacaggg gaatttagac gtgactaagt agcagtacat 900
atgaaaaatt attgaggaat tttgttgact ttaagggtag tgtgagtcaa cactgtgatt 960
tggtctccag aaaataaact caatccaagg ctgtatcaac aaaggcatac tgtccattct 1020
gcatgctcat tacagcacta agtaccgagc catgttctca accgcatact tcatgaacat 1080
ggaaagctaa cagtatggtt aaggggggaa actggaactg tcatcttggg gaataaaagg 1140
gatatttagc caggagtaaa gttagcttag ggagaccatg ataaatattt tcaaaatatt 1200
tgaaggactc agttgtggaa gtgagattag atttattgtg taaaactcca ggagtcaaaa 1260
gcaatagaga gatagaagga aatgcttttc agcagtgttg ctcatcaata aaggaggatga 1320
acagccacac agaatggaag gttccctgtc ctttgagata tttaagcctt caagtaaatt 1380
atgggtgagg agtttcaa atagagtga accagataag aaagtctctt cttccggtaa 1440
gatattatgg acctataaca tctgtgtact taaaagtaga ttgggagtga aaggcagact 1500
tttgatgttc tgtactgt tgaaaccct tagcgtggtc ctctgtaacc tgctcaccct 1560

gccccaaagga ggcagctagc caatgccacc agcccaacgg aaaccccagt gcttttccaa 1620
tggggaaatg cagtcacttt ttttggatg ctacacatcc tttctggaat atgtctcaca 1680
cacatctctc tttatcacc cttttttcaa gtaaaccaac ttcttgca gaagtgacaat 1740
gtgtctcttt actctccacg aagattctgg cctttctctt cacctgtcag aagtttagga 1800
ttccaaaggg atcattagca tccatcccaa cagcctgcac tgcactctga gaactgcggg 1860
tcttgatca tcaggcaact ttcaactaca cagaccaagg gagagagggg acccctccga 1920
ggccccatag ggttctctga catagtgatg acctttttcc aaactttgag cagggcgctg 1980
ggggccaggc gtgcgggagg gaggacaaga actcgggagt ggccgaggat aaagcggggg 2040
ctccctccac cccacggtgc ccagtttctc cccgctgcac gtggtccagg gtggtcgc 2100
cacctctaaa gccggtcccg ccaaccgcca gcccgggac tgaacttgcc cctccggccg 2160
cccgtcccc gcaggggaca ggggcgggga gggagagatc cagagggggg ctgggggagg 2220
tggggccgcc ggggaggagg cgagggaaac ggggagctcc agggagacgg cttccgaggg 2280
agagtgaag gggagggcag cccgggctcg gcacgctccc tccctcgcc gctttctctc 2340
acataagcgc aggcagagg cgctcagtc atgcctgcc cctgcgccc cgcgcgcgc 2400
cgccgctc cagcccggcg cgctctggag gatcctgcgc cgcggcgctc cccggccccg 2460
ccgcgcgcag cgcgcccg gcctctctc cgcgcccg caccgcccgc agcgcgcccg 2520
ccgcagcgc cgcggcccg ctctctcac ttcggggaag gggaggagg agggggacga 2580
gggctctggc gggtttggag gggctgaaca tcgcggggtg ttctggtgtc cccgccccg 2640
cctctccaaa aagctacacc gacggggacc gggcgggcgt cctccctcgc cctcgcttca 2700
cctcggggc tccgaatgcg gggagctcg atgtccggtt tctgtgagg cttttacctg 2760
acacccgcg ctttccccg gactggctg ggagggcgcc ctgcaaagt gggaacgcg 2820
agcccgga cgcctccgc cgctccggc tcgcccagg ggggtcgcc ggaggagccc 2880
gggggagagg gaccaggagg gggcgcggc ctgcaggg cgcccgccc cccacccctg 2940
ccccgcag cggaacggtc cccaccccc ggtccttcca ccatgcactt g 2991

<210> 49

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 49
cacggcttat gcaagcaaag

20

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 50
aacacagttt tccataatag

20

<210> 51
<211> 19
<212> PRT
<213> Homo sapiens

<400> 51
Leu Ser Lys Thr Val Ser Gly Ser Glu Gln Asp Leu Pro His Glu Leu
1 5 10 15

His Val Glu

<210> 52
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 52
gacggacaca gatggagggtt taaag

25

<210> 53
<211> 196
<212> PRT
<213> Homo sapiens

<220>
<223> Human PDGF-A

<400> 53
Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
1 5 10 15
His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
20 25 30
Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
35 40 45
Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
50 55 60
Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
65 70 75 80
Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
85 90 95
Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
100 105 110
Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
115 120 125
Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
130 135 140
Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
145 150 155 160
Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
165 170 175
Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
180 185 190
Thr Asp Val Arg
195

<210> 54
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Human PDGF-B

<400> 54
Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg
1 5 10 15
Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met
20 25 30

- 32 -

Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu
35 40 45
His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met
50 55 60
Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg
65 70 75 80
Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu
85 90 95
Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
100 105 110
Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln
115 120 125
Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
130 135 140
Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
145 150 155 160
Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
165 170 175
Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser
180 185 190
Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
195 200 205
Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
210 215 220
Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly
225 230 235 240
Ala

<210> 55
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<223> Human PIGF

<400> 55
Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
5 10 15
1

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Cys Gly Asp
130 135 140

Ala Val Pro Arg Arg
145

<210> 56

<211> 191

<212> PRT

<213> Homo sapiens

<220>

<223> VEGF165 precursor

<400> 56

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
180 185 190

<210> 57

<211> 188

<212> PRT

<213> Homo sapiens

<220>

<223> VEGF-B167

<400> 57

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
130 135 140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145 150 155 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
165 170 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
180 185

<210> 58
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: VEGF-C delta Cys156 mutant

<220>
<223> At position 156, "Xaa" can be anything other than cysteine or can be nothing

<400> 58
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
20 25 30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Xaa Val Ser Val Tyr
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
405 410 415

Gln Met Ser

<210> 59
<211> 160
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: VEGF-C delta N delta CHis

<400> 59

Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Thr
20 25 30

Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu
35 40 45

Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
50 55 60

Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr Phe
65 70 75 80

Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn
85 90 95

Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys
100 105 110

Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys Pro Val
115 120 125

Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu
130 135 140

Asp Val Tyr Arg Gln Val His Ser Ile Ile His His His His His His
145 150 155 160